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Perfect score:
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ALIGNMENTS

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RESULT 1
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Q9H8I7
Q9H8IA
DI Q9H8
AC Q1-M
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ISogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai T., Kaku Y., Kodaira H., Kondo H., Sugawara Nagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Swatanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Takiguchi Swatanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK02365; BAB14629.1; -.
SEQUENCE 330 AA; 38958 MW; EBA21A1AC1455C2E CRC64;
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Q9H817;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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MMNEQPPSKAWRASQMMTEFIELLEFPSETGVLCTLAITIWRLKPSADCGPERGLPLFIH
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NGCD; MGI:1921674; 4932443L08Rik.

SEQUENCE 757 AA; 87667 MW; 320D61A71CF51DAE CRC64;
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Best Local Similarity
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01-JUN-2001 (T)
4932443L08Rik |
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 5.1e-73;
6; Mismatches 18;
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01-MAY-2000 (
01-MAR-2002 (
                                  Submitted
EMBL; AK07
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SEQUENCE
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EMBL; BC018346; AAH18346.1; -.
InterPro; IPR000515; BPD_transp.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; SEQUENCE 444 AA; 50427 MW; DD4053A37
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; C
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                                                                              "The nucleotide sequence
                                                                                      Jikuya H., Takano
                                                                                              TISSUE-SPLEEN;
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                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.165; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 292.5;
Pred. No. 1.
                                                                             long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                 Craniata; Ve Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                INN_MEMBR; UNKNOWN_1.
DD4053A374A00FA1 CRC64;
                                    346FEE61A2C44B23 CRC64;
                                                                                      Kikuno
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annotation update)
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         2e-19;
                                                                              R., Na
                                                                                                                                           Vertebrata;
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les 63;
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on update)
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                                                                                                                                   Hominidae;
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isolated
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                  811;
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RESULT
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Best Local S
Matches 57
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Hypothetical
SEQUENCE 45
                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-DEC-2001 (TrEMBLrel. 19, La
Hypothetical 42.3 kDa protein
Mus musculus (Mouse)
                                                                                                                                                                                                                 Q99K19
Q99K19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ datalembL; BC004840; AAH04840.1; -.
EMBL; BC013502; AAH13502.1; -.
Interro; IPR000515; BPD_transp.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
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Q99J32;
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Similar to expressed in
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kDa protein).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTVWVRRLEHAGSGASWLPWLHHFLVENTFFLFLASALLLAVIYFNIQVVKGQRKVICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANCQAPRRPWLASHMSTVFLTLLCFPSFLGAAVFLCYAVWQVRPSSTCGPFRTLNTMYE
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                                                                                                                                                                                                                                                                                                                                            LKEQIRNEGEDKIFLINKLHSVYEEEGRSRP
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450 AA; 5
                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                Chordata;
Rodentia;
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Rodentia;
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17, Last sequence update)
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activated T/LAK lymphocytes
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Last sequence update)
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                                                              Craniata; Ver
Sciurognathi;
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                                                                Vertebrata;
chi; Muridae;
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; Murinae; Mus
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RESULT 7
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AC Q9H7
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DT 01-J
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DT 01-J
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OC Euk
OC Man
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Best Local S
Matches 40
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Best Local
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Q966F8
Q966F8;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Q9H766;
01-MAR-2001 (TIEMBLIFEL 16, Created)
01-MAR-2001 (TIEMBLIFEL 16, Last sequence up
01-MAR-2001 (TIEMBLIFEL 16, Last annotation
CDNA: FLJ21240 fis, clone COL01132.
                                                                                                                                                                                                                                                                                                                     Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Yokitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AKO24893; BAB15032.1; -
SEQUENCE 402 AA; 46254 MW; 716C111B5B794DC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ data EMBL; BC005510; AAH05510.1; -. EMBL; BC006956; AAH06956.1; -. InterPro; IPR000515; BPD_transp. PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 373 AA; 4
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                                                                                                                                  KIMIRLLHEQIINEGKDKMFLIEKLIKLQ-DM 144
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                                                                                                                                                                  TVSTFPSSLQSFIHGVTSE---
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36; Conserv
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                  PRELIMINARY;
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Pred. No. 0.00
29; Mismatches
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Pred. No. 1.1e
18; Mismatches
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les 46;
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Last sequence update)
Last annotation update)

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RESULT
Q8R4P4
ID Q8
AC Q
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                      TMC2.
TMC2.
Mus musculus (Mouse).
Mus musculus (Mouse).
Thervota; Metazoa; Chordata;
Thervota; Metazoa; Rodentia;
MEDLINE-21918583; PubMed-11850618;
Kurima K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Meno Deshmukh D., Oddoux C., Ostrer H., Khan S., Raizuddin S. Deininger P.L., Hampton L.L., Sullivan S.L., Battey J.F. Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.; "Dominant and recessive deafness caused by mutations of TMC1, required for cochlear hair-cell function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
Submitted (AUG-2001) to the EMBI
EMBL; AC006685; AAK84572.1; -.
SEQUENCE 1247 AA; 142928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metaz
Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R4P4;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R4P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode investigating biology. The C. electeristics 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
T13G4.3.
                                                                                                                                                                                                                     NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Favello T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSKAWRASQMMTFETFLLFFPSFTGVLCTLAI--TIWRLKPSADCGPFRGLPLFIHSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHFYTVVTREIEKRVDQTVLSYIRHIASPGVVIPIILFLILIIYFLFSLVRGLREANTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAREIFRASRSSNFYLGILL---IWLLLCTLPVGFVIASMSPSRSCGPF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAQLVHER---TEEKKKIFELAGGKKNKFEKDRD-KKRSNDYIPLIEQRRREPWRQYHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIRLLHEQIINEGKDKMFLI-----EKLIKLQDMEKKANPSSLVLERREVEQQGFLHLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
ne cochlear-expressed protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9851916
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) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T13G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.5; DB Pred. No. 0.11; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cosmid T13G4.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans
                                                                                                                                                                                                                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans: a platform for sequencing Consortium.
                                                                                                                                                                                                                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                           Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
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                                                                   lin S.,
J.F.,
                                                                                                              Menon
                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Mus
                          of a
                                                                                                                                    Z . M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ARY
                          novel
                                                                                                              Naz
P.S.
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                                                                                                            . N. ,
                        gene
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RESULT
Q9BYN5
ID Q5
AC Q5
DT 01
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AC Q8
AC Q8
AC Q8
AC Q8
DT Q1
DT Q1
DT Q1
DT Q1
DT Q1
DT Q1
CC Q8
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DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 43
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Best Local
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Q9BYN5
Q9BYN5;
Q9BYN5;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
DJ686C3.6 (NDJ686C3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
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EMBL; AF417581; AAL86402.1; -.
SEQUENCE 888 AA; 101134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 31.3 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8R1X9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820
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                                                                                                                                                                                                                                           CYGR--LISELKRQIETEVQNKVFLAQRAVAL
                                                                                                                                                                                                                                                                                                                               SIWAQIPEAIESLPQTAQNFLY-----FLGTQAF---
                                                                                                                                                                                                                                                                                                                                                                                                                      YSPASRTFRASTANFFFPLVL------LVGLAISAVPVLYSIFLIPPSKLCGPFRGKL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHSSSQIQTLDKKAQGPHTSSTEGGASPSTSWHHV----GSQPPRGRR--DSGQPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHERVEKASRSNNEYMGLLLLVLELSLL-PVAYTVMSLPPSEDCGPESGKNRMYDVLHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSKAWRASQMMTFFIFLLFFPSFTGVLCTLAITIWRLKPSADCGPFRG------
                                                                                                                                                                                                                                                                                    -EGRKIMIRLLHEQIINEGKDKMFLIEKLIKL
                                                                                                                                                                                                                                                                                                                                                                         LFIHSIYSWIDTL-STRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSKSLSRANAQLRKKIQALREVEKNHKSIKGKAIVTYSEDTIKNSSKNATQIHLTKEEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LPLFIHSIYSWIDTLSTRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LQDMEKKA-NPSSLVLERREVEQQGFLHLGEHDGSLDLRSRRSVQEGNPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IENDFPKFLGKIFAFL----ANPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tted (FEB-2002) to the BC022758; AAH22758.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                      (Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AA; 31318 MW;
                                         (TremBLrel. 17, Created)
(TremBLrel. 17, Last sequence up)
(TremBLrel. 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                      protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MIRLLHEQIIN----EGKDKMFLIEKLIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%;
28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.9%;
21.5%;
                          (Fragment)
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Pred. No. 0.46
33; Mismatches
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Pred. No. 0.22
Pred. Mismatches
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Sciurognathi;
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AA Kurima K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Na Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S. A Deshmukh D., Oddoux C., Ostrer H., Khan S., Raizuddin S., 'A Deininger P.L., Hampton L.L., Sullivan S.L., Battey J.F., 'A Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.; T "Dominant and recessive deafness caused by mutations of a nov. TTMC1, required for cochlear hair-cell function.";

L. Nat. Genet. 30:277-284(2002).

R. EMBL; AF417580; AAL86401.1; -.
SEQUENCE 890 AA; 101006 MW; A35AE2216B2ACOC4 CRC64:
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 29
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Best Local
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 Q97MN0;
Q97MN0;
01-OCT-2001
01-OCT-2001
01-OCT-2001
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001) to the EMBL; AL049712; CAC29096.1;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                               IENDFPTFLGKIFAFL---ANPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (Human).
                                                                                                                                                                                                             PHERVFKASRSNNFYMGLLLLVLFLSLL-PVAYTIMSLPPSFDCGPFSGKNRMYDVLQET 723
                                                                                                                                                                              ----LPLFIHSIYSWIDTLSTRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYW
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29; Conservative
                                                                                                                                                                                                                                                                                            Similarity
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                                                                  PRELIMINARY;
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Cochlear-expressed protein 2.
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24357 MW;
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Primates;
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Created)
Last sequence Last anno
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Pred. No. 0.8;
L8; Mismatches
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Pred. No. 0.18;
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sequence update)
annotation update)
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1.8;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wilming L., Wang K.H., Wan
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EMBL; AE007529; AAK78148.1; -.
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STRAIN-ATCC 824 / DSM 792 / VKM B-
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Clostridiaceae; Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQDMEKKANPSSLVLERREVE 161
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35; Conserv
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Pred. No. 0.69
32; Mismatches
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Hasegawa
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                        Wilming L.,
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Best Local S
Matches 34
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R MEDLINE-21918583; PubMed-11850618;

K WITIMA K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz A., Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S., Deshmukh D., Oddoux C., Ostrer H., Khan S., Raizuddin S., Deshmukh D., Oddoux C., Ostrer H., Khan S., Raizuddin S., Deshninger P.L., Hampton L.L., Sullivan S.L., Battey J.F., Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;

M Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;

"Dominant and recessive deafness caused by mutations of a nove TMC1, required for cochlear hair-cell function.";

Nat. Genet. 30:277-284(2002).

R EMBL; AF417579; AAL86400.1; -.

SEQUENCE 757 AA; 87264 MW; 9FB6CB73A7DD367D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.1%; Score 91.5; DB 11; Best Local Similarity 20.7%; Pred. No. 2.3; Matches 34; Conservative 27; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8R4P5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transmembrane cochlear-expressed protein 1.
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EMBL; AK016832; BAB30454.1; -.
MGD; MGI:1921712; 4933416G09Rik.
SEQUENCE 279 AA; 31965 MW; 71E4F324D407716E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                   --HSIYSWIDTL---STRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQIT-EGR 113
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